

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 15, 2003, 06:15:49 ; Search time 3999 Seconds
(without alignments)
10916.281 Million cell updates/sec

Title: US-09-043-944-5
Perfect score: 1500
Sequence: 1 gtttaattcccaagtgtga.....taaaaaaaaaaaaaaaaa 1500

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_hgt.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vl.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_ov.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vl.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1454.6	97.0	1461	3	CEU35660	U35660 Caenorhabdi
2	1311.8	87.5	1335	3	AF171064	AF171064 Caenorhab
3	631	42.1	27102	3	U41540	U41540 Caenorhabdi
4	276.2	18.4	1896	4	AF038936	AF038936 Bos tauru
5	268.2	17.9	2428	5	DRE132931	AJ132931 Danio rer
6	264.2	17.6	2607	5	D84427	D84427 Xenopus lae
7	261.6	17.4	1836	5	AY043492	AY043492 Gallus ga
8	261	17.4	1430	9	MPRSLN1	Z71333 M.murinus p
9	258.4	17.2	1407	10	RATSL182	D82578 Rattus norv
10	255.2	17.0	1407	10	D82363	D82363 Rattus norv
11	252.2	16.8	1241	5	CCPS1	Y17128 Cyprinus ca
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15	248.2	16.5	2764	6	AR095621	AR095621 Sequence
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17	248.2	16.5	2765	6	AX244648	AX244648 Sequence
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ALIGNMENTS

CEU35660 1461 bp mRNA linear INV 23-JAN-1996
Caenorhabditis elegans membrane protein (sel-12) mRNA, complete
cds.
U35660
U35660.1 GI:1109793

Caenorhabditis elegans.
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
Rhabditoidae; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 1461)
Levitani, D. and Greenwald, I.
Facilitation of lin-12-mediated signalling by sel-12, a
Caenorhabditis elegans S182 Alzheimer's disease gene
Nature 377 (6547), 351-354 (1995)
96032531
7566091
2 (bases 1 to 1461)
Levitani, D.
Direct Submission
Submitted (07-Sep-1995); Diane Levitan, Biochemistry, Columbia
University, 630 W. 168th St., New York, NY 10032, USA
On Dec 9, 1995 this sequence version replaced gi:1000566.
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RESULT 2

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 VERSION AF171064.1 GI:5759132
 KEYWORDS
 SOURCE
 ORGANISM
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 Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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 Eimer, S. and Baumeister, R.
 TITLE Caenorhabditis elegans presenilin SEL-12
 JOURNAL
 REFERENCE
 2 (bases 1 to 1335)
 Eimer, S. and Baumeister, R.
 AUTHORS
 TITLE Direct Submission
 JOURNAL
 Submitted (22-JUL-1999) Genzentrum, LMU Munich, Feodor-Lynen-Str.
 25, Munich 81377, Germany

FEATURES

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gene

CDS

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QY 327 TGAATGCTCTCGTCACTGTTGCGTGTGCTGATGACAGTCTTCTGCTGATGTTT 386
Db 5689 TGAATGCTCTCGTCACTGTTGCGTGTGCTGATGACAGTCTTCTGCTGATGTTT 5748

QY 387 CTATAAATCAAGCTTTTATAAGCTTATCATGATGCTTATTCAGACAGTCTTCTTCT 446
Db 5749 CTATAAATCAAGCTTTTATAAGCTTATCATGATGCTTATTCAGACAGTCTTCTTCT 5808

QY 447 TCTTTTCCATTTCACATCAATCTATGTGA-----476
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QY 477 -----AGAAAGTCTGAAAAGTTTCGATGTGTCTCCAGCGCACTATTGGT 521
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Db	717	TATCTGATCATGATACGCGCTCATGGCTCTGGTCTTCATCAAAATATCTCCCGAGTGG	776
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Db	1226	TAAAGCATCAGCTACAGCCAGCGGTGACTGGAAACAGCAGCTAGCGCTTCTGCGCCAT	1285
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Qy	1254	TCT-GCAATTTCCATTTTCTCCGAGCTCATTTTCTTTTACTTTTGTAC	1297
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LOCUS	D84427	2607 bp	linear
DEFINITION	Xenopus laevis mRNA for presenilin-alpha, complete cds.		
ACCESSION	D84427.1		
VERSION	D84427.1 GI:1943353		
KEYWORDS	presenilin-alpha.		
SOURCE	Xenopus laevis brain cDNA to mRNA.		
ORGANISM	Xenopus laevis		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;		
TITLE	Xenopus laevis		
JOURNAL	Cloning of Xenopus presenilin-alpha and -beta cDNAs and their		
MEDLINE	different expression in oogenesis and embryogenesis		
REFERENCE	Biochem. Biophys. Res. Commun. 231 (2), 392-396 (1997)		
AUTHORS	Tsujiyama, A.		

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02 TCTTCAATCTCATACCTTCGGGCTGTTTTCTACTTTGCCAC 1346

RATS182 1407 bp mRNA linear ROD 11-JAN-2002
Rattus norvegicus mRNA for S182 protein, complete cds.
D82578.1 GI:1139562

Rattus norvegicus (strain:Wistar) brain cDNA to mRNA.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

1 Taniguchi,T., Hashimoto,T., Taniguchi,R., Shimada,K., Kawamata,T.,
Yasuda,M., Nakai,M., Terashima,A., Koizumi,T., Maeda,K. and
Tanaka,C.
Cloning of the cDNA encoding rat Presenilin-1
Gene 186 (1), 73-75 (1997)
97199371

2 (bases 1 to 1407)
Taniguchi,T.
Direct Submission
Submitted (22-DEC-1995) Taizo Taniguchi, Hyogo Institute for Aging
Brain and Cognitive Disorders, Department of Neuroscience; 520
Saisho-ko, Himeji, Hyogo 670, Japan (E-mail:tanigu@hiabdc.go.jp,
Tel:0792-95-5311, Fax:0792-95-8199)
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DEFINITION	Rattus norvegicus mRNA for presenilin-1, complete cds.				
ACCESSION	D82363.1 GI:1777325				
VERSION	presenilin 1.				
KEYWORDS	Rattus norvegicus (strain:Wistar) embryo male brain cDNA to mRNA, clone:RPS-1.				
SOURCE	Rattus.				
ORGANISM	Rattus norvegicus				
REFERENCE	1 (sites)				
AUTHORS	Takahashi, H., Murayama, M., Takashima, A., Mercken, M., Nakazato, Y., Noguchi, K. and Imahori, K.				
TITLE	Molecular cloning and expression of the rat homologue of presenilin-1				
JOURNAL	Neurosci. Lett. 206 (2-3), 113-116 (1996)				
MEDLINE	96255262				
REFERENCE	2 (bases 1 to 1407)				
AUTHORS	Takahashi, H., Takashima, A.A. and Murayama, M.M.				
TITLE	Molecular cloning and expression of rat presenilin-1				
JOURNAL	Unpublished				
REFERENCE	3 (bases 1 to 1407)				
AUTHORS	Takahashi, H.				
TITLE	Direct Submission				
JOURNAL	Submitted (22-DEC-1995) Hiroshi Takahashi, Mitsubishi Kasei Institute of Life Sciences, Laboratory of Biochemistry, 11 Minamiooya, Machida, Tokyo 194, Japan (tel:0427-24-6211, Fax:0427-24-6314)				
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CDS					

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Query Match	17.08; Score 255.2; DB 10; Length 1407;				
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Matches 665; Conservative 0; Mismatches 538; Indels 37; Gaps 5;					
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Qy	578	GTCAATGTGCTGCAACAGTTCTACCTTATTAACAATGTCGCACTAAATGGCTCTGCT	637		
Db	650	GCCCACTCCGACHTGAGGCGTATCTCATATGATGATGAGTCCCTCACTGCTCGTAT	709		
Qy	638	TTATCAAGTACCTCCCTGAAATGACCGCATGGCTATCTTGGCTGTGATTCAGTATAG	697		
Db	710	TTATCAAGTACCTCCCTGAAATGACCGCATGGCTATCTTGGCTGTGATTCAGTATAG	769		
Qy	698	ATCTGTTGCGTGTACACCAAAAGGACCATTTGATATTTGTTGGAACCTGCACAGG	757		
Db	770	ATTTGTTGCTGTCTGTGCCCCAAAGTCCACTTGTATGCTGTGTCGAAACAGCTCAGG	829		
Qy	758	AGAGAAACGAGCAATTTTCCGGCGCTGATTTATTCGTCTGGAGTCATCTATCCCTACG	817		
Db	830	AAAGAAATGAGACTCTCTTTCCAGCTCTTATCTATCTTCTCAACCATGTTGTTGGTGA	889		
Qy	818	TTCTGTTTACTGCAAGTTGAAAACACAGACAGACCCCGTGAACCGACGTCGTGACACTCA	877		
Db	890	ATATGSGCT-----GAAGGACACCCAGAAAGCCCAAGAGGAGGTACCCCAA	932		
Qy	878	ATACTTCTACAGCTTTTCTGAGAGCGGAGTGTGTTCTATCTCAAGCCGCAACAGGCCAA	937		
Db	933	AAACCCCAAGTATAGCACAGAGACAGAGAGGGAAGACACAGGACACTGGCAGCTGG	992		
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Db	993	GAGCGATGATGTTGCTTCAAGTGGAGTGGGAGGCCCAAGAGACAGTCACTCTGGGCC	1052		
Qy	998	AAAACCTGGAGTANGGTGGAAACGGGAGCTAGCTGCTGAGACCAACTGTACAGAGC	1057		
Db	1053	TCATCGCTCCACT-----CCTGAGTCAAGAGCTGCTGTCCAGGAACCTTCTCTGGA	1102		
Qy	1058	CCAATTTTACAGGACGAAAGGAAGAGAGAGTGTGNAACCTTGCTGGCGCACTTCA	1117		
Db	1103	GCATCTCTCACTAGTGAAGACCCCGAGAGAGAGAGTGAAGCTTGGCTGGGAGATTCA	1162		
Qy	1118	TTTTTCTACTCTGTTCTCTCGCAAGGCTTCATGCTAC-----TTTGAAGTGAACACGA	1171		
Db	1163	TTTTTCTACAGTGTCTGTTGTTGAAGGCTTCAGGACCCGAGTGGGAGCTGGAACACA	1222		
Qy	1172	CTATCGCTTCTTATGTCGCAATTTATTCGCTCTCTGCTTCATCTTGTCTCTGCTCGCG	1231		
Db	1223	CCATAGCTCTGTTTGTAGCCATATGATCGGCTGTGCTTACTTACTCTCTGCTCGCCA	1282		
Qy	1232	TCTTAAACGAGCACTCCCGGCTC-TGCAATTTTCCATTTTCTCCGAGCTCATTTTTTACT	1290		
Db	1283	TTTTCAAGAAAGCTTTCGCGCCCTTCCCATCTCCATCACTTCGGGCTCATTTTCTACT	1342		
Qy	1291	TTTGTACCGCTGATCATCACCCCATTTGTTTACAAAGT	1330		
Db	1343	TTGCCAGGATTATCTCGTGCAGCCCTTCATGACCAACT	1382		
RESULT 11					
CCPS1					
LOCUS	Cyprinus carpio mRNA for PS1 protein.				
DEFINITION	Cyprinus carpio mRNA for PS1 protein.				
ACCESSION	U17128				
VERSION	U17128.1 GI:3087753				
KEYWORDS	PS1 gene.				
SOURCE	common carp.				
ORGANISM	Cyprinus carpio				
REFERENCE	1 (bases 1 to 1241)				
AUTHORS	Archer, S., Hirano, J., Diss, J. K., Fraser, S. P. and Djamgoz, M. B.				
TITLE	Expression and localization in the fish retina of a homologue of				
JOURNAL	the Alzheimer's related PS1 gene				
MEDLINE	Neuroreport 9 (9), 2049-2056 (1998)				
PUBMED	98337349				
REFERENCE	2 (bases 1 to 1241)				
AUTHORS	Archer, S. N.				
TITLE	Direct Submission				
JOURNAL	Submitted (14-APR-1998) S. N. Archer, International Marine Centre,				
FEATURES	Localita sa Mardini, 09072 Torreggande, Oristano, ITALY				
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	/note="variant"				
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QY	598	T	TCTACCTTATTACAACTGCTGCACATAATGGCTCTGGTCTTTATCAAGTACCTACCGAA	657
Db	428	G	CCATCTGATCATGATCAGCGCTCTAATGGCCCTGGTCTTCATCAAGTACTCTCCGGAG	487
QY	658	T	GGACTGTGTGGTTGTGCTGTTTCTGTTATCTCTCGGTTTGGGATCTGGTTCGCGTGTCA	717
Db	488	T	GGACCGCTCGCTCATCTCGCTGCTATATCTGCTACGATCTGTGGCCGCTGTGTGC	547
QY	718	C	CAAAAGGACCAATTGAGATATTTGGTGGAACTGCACAGGAGAGAAAGAGCCAAATTTTC	777
Db	548	C	CGAAAGACCCCTTCGCTATCTCTTGTGGAAACGGCTCAAGAGAGGAATGAACCCATCTTC	607
QY	778	C	CGCGCGTGATTTATTGCTCTGGAGTCACTCATCCCTACGTTCTTGTACTGCAAGTTCAA	837
Db	608	C	CTGCTCTCATCTACTCCTCAACCATGGTGTGGCTGTTTAATATGGCGGACGCGCAGAG	667
QY	838	A	ACAGCAGACACCCCGTGAACCGACGCTGCTGACACTCAATATCTTACAGCTTTTCCCT	897
Db	668	C	CCAGGAATAATTCCAGCA-----TCCAGTTCCCTCAG	700
QY	898	G	GGAGCGGAGTGTGTCATCTGAAACGCCAAAGCGCCAAAGTGAACGAATTTCTCTCAA	957
Db	701	C	CAGAGAACCGAGATGCGGTGGCACCCACCGCTCAGCCGGAGGATGATGCGGTTTCACA	760
QY	958	A	AGTGCAAATPCGAATCGAATCTACAGCTTCAACGACACAAAACTCTGGAGTAAAGGTG	1017
Db	761	C	CAAGCTGGGTGTC-----AATCAGCAGCAGCATCAGCTCGGCCCATGCAGTCCACTGA	813
QY	1018	G	ACGGGAGCTAGTCTGAGAGACCAACTGTACAAACGCGCAATTTTACAGGCACGAA	1077
Db	814	G	CAGCAGCAGAGAGATCCAGAGCTGCCCTCC--GCACGCCCGCCACCTGTGGAAGAC	871
QY	1078	G	AGGAGAGAGAGGTGTGAACCTTGGTCTCGGGGACATTCAATTTTCTACTCTGTCTCTCTC	1137
Db	872	G	AGCAGAGCGGGGTGTGAAGCTGGGTTTGGAGATTTTCATCTTTTACAGTATGCTGGTG	931
QY	1138	G	GCATCTCGTACTTTGACTTGAACAGCACTATCGGTTGTTATGTTGTCGCT	1191
Db	932	G	GTAAGCATCAGCTACAGCCAGCGGTGACTTGAACACAGCAGTAGCCTCTTGTGGCC	991
QY	1192	A	TTCTTATCGGTCTCTGCTTCACTCTGTCTGCTCGCGCTCTTCAACAGCAGCTCCCG	1251
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QY	1252	G	CTCT--GCAATTTCCATTTTCTCCGAGCTCATTTTTTACTTTTGTACCCGCTGGATCATC	1310
Db	1052	G	CTCTCCCCATCTCCATAAGCTTCGGCCCTGGTCTTTTACTTTGCCACCGATAACCTCGT	1111
QY	1311	A	CCCCATTTGTTACAAAGTCTCTCAAAAGTGTTTATATATTAATTTCTGTTTTTGGC	1370
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QY	1371	A	TTTCTTTGCATCATCAACTTTTTCGATTTATATCTTGAGCGATCTCAAG	1419
Db	1172	A	CTCCTCGTCGGCTTTCACCTTTACAGCTAATTTCCAGAAATCCTCTTCGAC	1220

RESULT 12
HSU40379
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

HSU40379
Human presenilin I-463 (AD3-3) mRNA, complete cds.
U40379
U40379.1 GI:1244637
.
Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1392 bp mRNA linear
(AD3-3) mRNA, complete cds.

PRI 12-AUG-1996

REFERENCE	1 (bases 1 to 1392)
AUTHORS	Sahara,N., Yahagi,Y., Takagi,H., Kondo,T., Okochi,M., Usami,M., Shirasawa,T. and Mori.H.
TITLE	Identification and characterization of presenilin I-467, I-463 and I-374
JOURNAL	FEBS Lett. 381 (1-2), 7-11 (1996)
MEDLINE	96193901
PUBMED	8641442
REFERENCE	2 (bases 1 to 1392)
AUTHORS	Shirasawa,T.
TITLE	Direct Submission
JOURNAL	Submitted (07-NOV-1995) Takuji Shirasawa, Molecular Pathology, Tokyo Metropolitan Institute of Gerontology, 35-2 Sakae-cho, Itabashi-ku, Tokyo, 175, Japan
FEATURES	Location/Qualifiers source 1..1392 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="14" /map="14q24.3" /clone="AD3-3" 1..1392 /gene="AD3-3" 1..1392 /gene="AD3-3" /codon_start=1 /product="presenilin I-463" /protein_id="AAB05894.1" /db_xref="GI:1244638" /translation="MTPELPAPLSYFQNAQMSDNHLSTNNDNRERQHNDRRSLGHP PLNGRPGNSRVQVDEDEELTLYGAKHVIMLFVPVTLCMVVVATIKSVSFY TRKDGQLIYPTFDDETGVQRALHSILINAAIMISIVMNTILLVLYKYRCYKVLRQ WLIISLLLEFFSYFLGVGFYTVAVDYITVALLINFGVGMISLHWKGPLRLQ QAYLIMISALMALVFYIKLPETAWILAVISVDLVAVLCPKGPLRMVLVTAQERNE TLPALITYSTMVLMNMAGDPDAORRSVKSNYNASTERESQDTVAENDDDGGSE EWEARQDSHLGPHRSTPESRAAQVELESSSLAGEDPEERGVLKLGDIFYFSVLVGKA SATASGDWNITIACFVAILLGICLTLLLILAIFKALPALPISITFGLVFFVFATDYLVLQ PFMDQLAFHFQYII"
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CDS	
BASE COUNT	359 a 310 c 333 g 390 t
ORIGIN	
Query Match	16.5%; Score 248.2; DB 9; Length 1392;
Best Local Similarity	54.6%; Pred.No.3e-46;
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QY	239 TTTTATAGTCAAAACAATGGAAGGCACTTACTATCACATCCTTTTGTCCGGGAACACAGA 298
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QY	479 AAGTTCTGAAAAGTTTCGATGTGCTCCAGCGCACTATGTGTTTGTGTTGTTGTTGTTGTTG 538
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Qy	659	GGACTGTGGTTTGTGCTGTTTGTATCTCGTTCGGTTCGTTGCGCTGCTGCAC	718
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Qy	719	CAAAAGACCAATTGAGATATTTGTTGGAACCTGCACAGGAGAGAAACGAGCAATTTTCC	778
Db	779	CGAAAGTCCCACTTCGTATGCTGTGTTGAAACAGCCAGGAGAGAAATGAACGCTTTTTC	838
Qy	779	CGGCGCTGATTTATTCGTCGTGGAGTCATATCCCTACGTTCTTTGTTACTGCACTGAAA	838
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Qy	899	GAGAGGCGAGTTGTTTCACTCAACAGCCAAACGGCCAAAGTGAACAGTAATCCTCAAA	958
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Qy	1312	CCCCATTTGTTACACAAGT	1330
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RESULT	13
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LOCUS	linear PAT 28-AUG-2001
DEFINITION	Sequence 3 from Patent WO0151671.
ACCESSION	AXI95267
VERSION	AXI95267.1 GI:15385819
KEYWORDS	. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Etheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	Mccarthy,J. and Cordell B. 1 (bases 1 to 1404)
AUTHORS	.
TITLE	Methods for identifying inhibitors of neuronal degeneration
JOURNAL	Patent: WO 0151671-A 3 19-JUL-2001;
	Scleros Inc. (US)

[illegible]

Df 1609 AGCCTTTTATGACCAATT 1627

RESULT 17
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LOCUS AX244648
DEFINITION Sequence 4 from Patent WO0167097:
ACCESSION AX244648
VERSION AX244648.1 GI:15859540
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Hale,R.S., Rowley,A.G. and Blackstock,W.G.
TITLE Novel assay
JOURNAL Patent: WO 0167097-A 4 13-SEP-2001;
GLAXO GROUP LIMITED (GB)
FEATURES
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BASE COUNT 715 a 624 c 652 g 773 t 1 others
ORIGIN

Query Match 16.5%; Score 248.2; DB 6; Length 2765;
Best Local Similarity 54.6%; Pred. No. 3e-46;
Matches 666; Conservative 0; Mismatches 513; Indels 40; Gaps 7;

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Qy 179 TATTGTGCCGGTGTCACATGCATCGCTGTGGTGTGTTTTACGATGAACACGATTACGT 238
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Qy 239 TTATATAGTCAAAACATGAAGGCATTTTACTATCATCATCCTTTTGTCCGGGAAACAGACA 298
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RESULT 20				
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LOCUS				
DEFINITION	AR060154	2791 bp	DNA	
ACCESSION	Sequence 133 from patent US 5840540.		linear	PAT 29-SEP-1999
VERSION	AR060154			
KEYWORDS	AR060154.1	GI:5986604		
SOURCE	.			
				Unknown.

[illegible]

[illegible]

Unclassified.

REFERENCE 1 (bases 1 to 2791)
 AUTHORS St. George-Hyslop, P. H., Rommens, J. M. and Fraser, P. E.
 TITLE Methods for determining risk of developing alzheimer's disease by
 detecting mutations in the presenilin 1 (PS-1) gene
 JOURNAL Patent: US 6194153-A 133 27-FEB-2001;
 FEATURES Location/Qualifiers
 source 1..2791
 BASE COUNT 742 a 624 c 652 g 773 t
 ORIGIN
 Query Match 16.5%; Score 248.2; DB 6; Length 2791;
 Best Local Similarity 54.6%; Pred. No. 3e-46;
 Matches 666; Conservative 0; Mismatches 513; Indels 40; Gaps 7;

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Qy 179 TATTGTGCGGCTGCTCACTATGCTTGCTGTGGTGTGTTTACCAGTAACACGATTACGT 238
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Qy 239 TTTATAGTCAAAACAATGAAGGCAATTTACTATACACATCCCTTTTGTCCGGGAAACAGACA 298
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Qy 299 GTATCGTTGAGAAGGATTGATGCACCTTGGAAATGCTCTCGTCTCATGTTGTGCGTGGTCG 358
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Qy 619 CTGTGGCGCAGAGAGCCCTGCACATCTGGAATGCTGCCATCATGATCAGTCAGTCATG 678
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Qy 479 AAGTTCTGAAAAGTTTCGATGTGTCCTCCACGCGACATATGGTTTTGTTGGACTGGGTA 538
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Qy 1201 AAAGCAGAAAGGGAGTC--ACAAGACATGTTGCAGAGAATGATGATGGCGGTTTCAG 1258
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AR144597			
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DEFINITION			
ACCESSION			
VERSION			
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AUTHORS			
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Db 1383 CAGAGGAAGGGAGTAAACTTGGATTGGAGATTTCTTTTCTACAGTCTCTCTGTTG 1442
QY 1139 GCAAGGCTT-----CATGCTACTTTTGTGCTGGAACAGACTATCGCTTGTATGTCGA 1192
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RESULT 25
AX418176

LOCUS AX418176 1404 bp DNA linear PAT 18-JUN-2002
DEFINITION Sequence 1 from Patent.WO0202601.
ACCESSION AX418176
VERSION AX418176.1 GI:21523186
KEYWORDS human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1
AUTHORS Carter,D.B. and Tomasselli,A.G.
TITLE Mutant presenilin 1 and presenilin 2 polypeptides
JOURNAL Patent: WO 0202601-A 1 10-JAN-2002;
PHARMACIA & UPJOHN COMPANY (US)

FEATURES

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/db_xref="taxon:9606"
772..777
/note="site directed mutagenesis sites"

BASE COUNT

361 a 312 c 335 g 390 t 6 others

ORIGIN

Query Match 16.5%; Score 247; DB 6; Length 1404;
Best Local Similarity 54.4%; Pred. No. 5.7e-46;
Matches 663; Conservative 0; Mismatches 516; Indels 40; Gaps 7;
QY 119 AAGAGGAAATGTTGTGGAAGACGGAGCTGAAATACGGAGCATCTCACGTTATTCATC 178
Db 194 AAGATGAGGAAGATGAGGAGCTGACATTTGAAATATGGCCCAAGCATGTGATCATGC 253
QY 179 TATTTGTCGGCTGTCACATGTCATGCTGCTGTTGTTTACGATGAACAGCATTCAGT 238
Db 254 TCTTTGTCGGCTGTCACATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 313
QY 239 TTTATAGTCAAAACAAATGAAGGCAATTTTACTATACATCATCTTTTCTCCGGGAAACAGACA 298
Db 314 TTTATACCGGAGGATG--GGCAGCTAACTATATACCCCATTCACAGAGATACCGAGA 370
QY 299 GTATCGTTGAGAGGATGATGTCACCTTGGAAATGCTCTCGTCAATGTTGTGCGGTGTCG 358
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Db 431 TTGTCATGACTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 490
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Db 611 ATTTTGGTGTGGTGGGAATGATTTCCATTTCACTGGAAGGTCCTTCCGACTCCAGCAGG 670
QY 599 TCTACCTTATPACAATGTCGCTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 658
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QY 1312 CCCCAATTGTTACACAGT 1330
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RESULT 27

LOCUS AR060024

DEFINITION Sequence 1 from patent US 5840540.

ACCESSION AR060024

VERSION AR060024.1 GI:5986474

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2791)

AUTHORS St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E.

TITLE Nucleic acids encoding presenilin II

JOURNAL Patent: US 5840540-A 1 24-NOV-1998;

FEATURES

Location/Qualifiers

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/organism="unknown"

BASE COUNT 742 a 623 c 654 g 771 t 1 others

ORIGIN

Query Match 16.4%; Score 246.6; DB 6; Length 2791;
 Best Local Similarity 54.6%; Pred. No. 7e-46;
 Matches 665; Conservative 0; Mismatches 514; Indels 40; Gaps 7;

QY 119 AAGACGAAATCTGTGGAAGAGCGGAGCTCAATACGAGCATCTCAGCTTATTCATC 178

Db 443 AAGATGAGCAAGATGAGGAGCTGACATTAATATGCGCCCAAGCATGTGATCATGC 502

QY 179 TATTTGCGCGGTGTCATGATCGCTCTGGTGTGTTTACGATGAACAGATTACGT 238

Db 503 TCTTTGTCCTGACTCTCTCATGGTGTGCTGCTGCTACCATTAGTCAGTCAGCT 562

QY 239 TTTATAGTCAAAACATGGAAGGCAATTTACTATACATCTCTTTTGTCCGGGAAACAGACA 298

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Db 620 CTGTGGCCAGAGACCCCTGCACTCAATCTGAATGCTGCCATCATGATCATGTCATG 679

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Db 800 AAGTGTAAACCTATACCTGCTGTGGACTACATTTACTGTTGTCACCTCTGATCTGGA 859

QY 539 ACTATGAGTTCTCGGAATGATGTATACATTTGGAAGGTCCTATGCTCTGCAACAGT 598

Db 860 ATTTGGGTGTGGTGGGAATGATTTCCATCTACTGAAAGGTCCTGCTGCTGCAAGCAGG 919

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QY 719 CAAAGGACCATTTGAGATATTTGTTGGAACCTGACAGGAGAGAAACAGCCTATTTTCC 778

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RESULT 28

LOCUS AR087179

DEFINITION Sequence 1 from patent US 5986054.

ACCESSION AR087179

VERSION AR087179.1 GI:10013942

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2791)

AUTHORS St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E.

TITLE Genetic sequences and proteins related to alzheimer's disease

JOURNAL Patent: US 5986054-A 1 16-NOV-1999;

FEATURES

Location/Qualifiers

1..2791

/organism="unknown"

BASE COUNT 742 a 623 c 654 g 771 t 1 others

ORIGIN

Query Match 16.4%; Score 246.6; DB 6; Length 2791;
 Best Local Similarity 54.6%; Pred. No. 7e-46;
 Matches 665; Conservative 0; Mismatches 514; Indels 40; Gaps 7;

QY 119 AAGACGAAATCTGTGGAAGAGCGGAGCTCAATACGAGCATCTCAGCTTATTCATC 178

Db 443 AAGATGAGCAAGATGAGGAGCTGACATTAATATGCGCCCAAGCATGTGATCATGC 502

QY 179 TATTTGCGCGGTGTCATGATGCTGTTGTTTGTGTTTGTGTTTGTGTTTGTGTTTGTGTT 238

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[illegible]

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DEFINITION	Sequence 5 from patent US 5840540.		
ACCESSION	AR060026		
VERSION	AR060026.1	GI:5986476	
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SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 3087)		
AUTHORS	St. George-Hyslop, P. H., Rommens, J. M. and Fraser, P. E.		
TITLE	Nucleic acids encoding presenilin II		
JOURNAL	Patent: US 5840540-A 5 24-NOV-1998;		
FEATURES	Location/Qualifiers		
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Best Local Similarity	54.6%;	Pred. No. 7e-46;	
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Qy	419	GATGGCTTATTTGTCAGCAGGTTTTCTTCTTTTCTTCTTCTACTACATACTATGTCGAAG	478
Db	1036	CCTGGCTTATATATCATCTCATTTGCTGTCTTTTTCATTTCTACTTTACTTGGGG	1095
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Qy	539	ACTATGAGTTCFCGGAATGATGTGTATACATTTGGAAGGTCATGCTCTGCAACAT	598
Db	1156	ATTGGTGTGGTGGGAATGATTTCCATTCAGTGGAAAGGTCCACTTCGACTCCAGCAGG	1215
Qy	599	TCTACCTTATTAACAATGCTGCACTAATGGCTCTGGCTTTTATCAAGTACCTACAGAT	658

		QY	1193	TTCCTATCGGTCTGCTTCACTCTTGCTGCCTGCCGGCTTTCAAACGAGCATCCCGG	1252
		Db	1786	TATTAAATGGTTGTGGCCTTACATAATTAATCTGCTTGCATTTTCAAGAAAAGCATTCGCCAG	1845
		QY	1253	CTCTG-CAATTTCCATTTTCTCCGGACTCATTTTTACTTTTTGTACCCTCGATCATCA	1311
		Db	1846	CUCITCCAANTCTCAATCACCTTTGGGCTGTTTCTACTTTGCCACAGATTATCTTGTTAC	1905
		QY	1312	CCCCATTTGTTACACAAGT	1330
		Db	1906	AGCCTTTTATGACCAATT	1924
RESULT 34					
ARI34368					
LOCUS	ARI34368			3087 bp	DNA linear PAT 16-MAY-2001
DEFINITION	Sequence 5 from patent US 6194153.				
ACCESSION	ARI34368				
VERSION	ARI34368.1 GI:14123273				
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 3087)				
AUTHORS	St. George-Hyslop,P.H., Rommens,J.M. and Fraser,P.E.				
TITLE	Methods for determining risk of developing alzheimer's disease by detecting mutations in the presenilin 1 (PS-1) gene				
JOURNAL	Patent: US 6194153-A 5 27-FEB-2001,				
FEATURES	Location/Qualifiers source 1..3087 /organism="unknown"				
BASE COUNT	789 a 688 c 740 g			866 t 4 others	
ORIGIN					
Query Match	16.4%;			Score 246.6; DB 6; Length 3087;	
Best Local Similarity	54.8%;			Pred. No. 7e-46;	
Matches	665; Conservative 0; Mismatches 514; Indels 40; Gaps 7;				
QY	119 AAGACGAAAAATGTTGTGAAGAAGCGAGCTCAAATACGGAGCATCTCACGTTATTTCATC	178			
Db	739 AACATGAGGAAGAAGATGAGGAGCTGACATGGAATATGGCCNAGCATGTGATCATGC	798			
QY	179 TATTGTGCGGTGTCACATCATGCATGGCTTGTTGTTTTACGATGAACACGATTACGT	238			
Db	799 TC TTTCCTCTGTGACTCTCTGCATGGTGGTGGCTGCCTACCATTAAAGTCAGTCAGCT	858			
QY	239 TTTATAGTCAAAACATGAAGGCATTTACTATACATCCTTTTGTCCGGGAACAGACA	298			
Db	859 TTTTATACCGAAGGATG---GGCAGCTAAATCTATACCCTTACAGAAAGATACCCGAG	915			
QY	299 GTATCGTTGAGAAGGATTGATGTGCATTTGAAATGCTCTCGTATGTTGTGGTGCTCG	358			
Db	916 CTGTGGCCAGAGAGCCCTGCACTCAATCTGAAATGCTGCCATCATGCAGTGTCAATG	975			
QY	359 TTCTGATGACAGTTCGTCTGATGTTTCTATAAATAACAAGTTTATAAGCTTATTTCATG	418			
Db	976 TTGTCATGACTATCTCTCTGGTGGTTCGTATAAATAACAGCTGCTATAAGGTCATCCATG	1035			
QY	419 GATGCTTATTTCTCAGCAGTTCCTCTCTCTTTTCCTTATTCACATPACAAATCTATGTGCAAG	478			
Db	1036 CTTGGCTTATTAATATFATFCATCTATGTTGCTGTTCTTTTTTTCATTTACTTGGGG	1095			
QY	479 AAGTTCTGAAAAGTTTCGATGTGCTCCCACGCGACATATTGGTGTGTTGGACTGGTA	538			
Db	1096 AAGTCTTTAAACCTATPACCTTCTGCTGGACTACATTAATGTTGCACTCCTGATCTGA	1155			
QY	539 ACTATGGAGTTCTCGGAATGATGTATACATTGGAAAGGTTCCTATGCGTCTGCAACAGT	598			
Db	1156 ATTTGGGTGTGGTGGGAATGATTTCCATTCACTGGAAAGGTCCACTTCGACTCCACAG	1215			
QY	599 TCTACTCTTATACAAATGTCGCACTAATGGCTCTGGTCTTTTATCAAGTACCTAACAGAA	658			

Db	1216	CATATCTCATTTATGATTAGTGCCCTCATGCCCTGGTGTATTATCAAGTACCTCCCTGGAAT	1275
QY	659	GGACTGTGTGGTTGTGCTGTTTCTATCTCGGTTTCGGAGTCTGGTTGCCGTGCTCACAC	718
Db	1276	GGACTGGTGGCTCATCTTGGCTGTGATTCAGTATATGATTTAGTGGCTGTGTTTGTGTC	1335
QY	719	CAAAAGAGCAATTCAGATATTTGGTGGAAACTGCACAGAGAGAAAACGAGCCAAATTTCC	778
Db	1336	CGAAAGGTCACACTTCGTATGCTGGTTCGAAACAGCTCAGGAGAGAAATGAACGCTTTTC	1395
QY	779	CGGCGCTGATTTATTCGTCCTGGAGTCACTATCCCTACGTTCTTTGTTACTGTCAGTTGAAA	838
Db	1396	CAGCTTCATTTACTCTCTCAACAAAT-----GGTGTGGTTGGTGAATATGGCA	1442
QY	839	ACACGACAGACCCCCGCTGAACCGACGTCGTCAGACTCAAACTCTCTACAGCTTTTCCCTG	898
Db	1443	GAAGGAGA----CCCCGAGCTCAAGGAGAGTATCCAAAATATCCAGTATTAATGTCAG	1497
QY	899	GAGAGGCGAGTTGTTCATCTCTGAAACGCCAAAGCGCCAAAGTGAACACGAATTCCTCAAA	958
Db	1498	AAAGCAGAGAAAGGGAGTGC--ACAAGACACTGTTGCAGAGAATGATCATGGCGGTTTCAG	1555
QY	959	AAGTGCAAATCGAATCGAATACTACAGCTTCAACGACACAAAACTCTGGAGTAAGGTGG	1018
Db	1556	TGAGGAATGGGAAGCCCCAGAGGACAGTCACTATAGGCGCTCATCTGCTCTACACCTCAGTC	1615
QY	1019	AACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAGACGCAATTTTCACAGGCACGAAG	1078
Db	1616	ACGAGCTGCTGTCCAGGAACCTTTCCAGCAGTAT-----CCTCGCTGGTGAAGACC	1665
QY	1079	AGGAAGAGAGAGGTGTGAAACTTTGGTCTGGCGCACTTCATTTTCTACTCTGTCTCCTCG	1138
Db	1666	CAGAGGAAAGGGGAGTAAACTTGGATGGGAGATTCATTTTCTACAGTGTCTGGTTG	1725
QY	1139	GCAAGGCTT-----CATCGTACTTTTCTACTGGAAACACGACTATCGCTGTATGTGGCCA	1192
Db	1726	GTAAAGCCTCAGCAACAGACGCCAGTGGAGACTTGGAAACACACCATAGCCTGTTTCGTAGCCA	1785
QY	1193	TTCTTATTCGCTCTCTGCTTCACTCTTGTCTGCTCGCGCTCTTCAACAGCAGCACTCCCG	1252
Db	1786	TATTAATTTGGTTTGTGCGCTTACATTAATTAATCTCTCGCTATTTCAAGAAAGCATTGCCAG	1845
QY	1253	CTCTG--CAATTTCCATTTTCTCGGAGCTCATTTTCTACTTTTGTACCCCGCTGGATCAATCA	1311
Db	1846	CTCTTCCAATCTCCATCACTTTGGGCTGTGTTTCTACTTTGCCACAGATTAATCTGTAC	1905
QY	1312	CCCCATTTGTTACACAAGT	1330
Db	1906	AGCTTTTATGGACCAATT	1924

RESULT	35
ARI144469	
LOCUS	ARI144469
DEFINITION	Sequence 5 from patent US 6210919.
ACCESSION	ARI144469
VERSION	ARI144469.1 GI:15106336
	3087 bp DNA linear PAT 08-AUG-2001

KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 3087)
TITLE	St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E.
JOURNAL	Genetic sequences and proteins related to alzheimer's disease
FEATURES	Patent: US 6210919-A 5 03-APR-2001;
source	Location/Qualifiers 1..3087

BASE COUNT	789 a	688 c	740 g	866 t	4 others
ORIGIN	/organism="unknown"				

Query Match	16.48;	Score 246.6;	DB 6;	Length 3087;
Best Local Similarity	54.68;	Pred. No. 7e-46;		

Qy	1193	TTCTATACGGTCTCTGTCTTCACTCTTGTCTGCTGCGCTTTCAAACGAGCACTCCCGG	1252
Db	1786	TATTAATTTGTTTGTGCTTACATTATTACTCTTGCCATTTTCAGAAAGCATTTGCCAG	1845
Qy	1253	CTCTG-CAATTTTCATTTTCTCGGACTCAATTTTTTACTTTTGTACCGCTGGATCATCA	1311
Db	1846	CTCTTCCAATCTGCATCACCTTTTGGGCTTGTTCCTTCTACTTTGCCACAGATTACTTGTAC	1905
Qy	1312	CCCCATTTGTTACACAGT	1330
Db	1906	AGCCTTTTATGGACCAATT	1924

RESULT	36
AR060155	
LOCUS	1962 bp DNA linear PAT 29-SEP-1999
DEFINITION	Sequence 135 from patent US 5840540.
ACCESSION	AR060155
VERSION	AR060155.1 GI:59866005
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1. (bases 1 to 1962)
AUTHORS	St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E.
TITLE	Nucleic acids encoding presenilin II
JOURNAL	Patent: US 5840540-A 135 24-NOV-1998;
FEATURES	Location/Qualifiers 1..1962 /organism="unknown"
source	
BASE COUNT	503 a 503 c 496 g 460 t
ORIGIN	

	Query Match	16.28;	Score 243.2;	DB 6;	Length 1962;
	Best Local Similarity	54.4%;	Pred. No. 4.2e-45;		
	Matches 644;	Conservative 0;	Mismatches 498;	Indels 42;	Gaps 6;
QY	116	AAGAGACGAAATGTTCGGAAGAAGCGGAGCTGAAATACGAGAGCATCTCACGTTATTTC	175		
Db	376	AACHAGATGAGGAGGAAGACGAAGACTGCACATTGTAATATGGAGCAAGCATGTGCATCA	435		
QY	176	ATCTATTGTGCCGGTCTCACTATGCATGGCTCTGCTTGTTTTTACGATGACACGATT A	235		
Db	436	TGCTCTTTGTCCCGTGACCCTCTGCATGGTCGTCTGGCCACCACATAAATCAGTCA	495		
QY	236	CGTTTTATAGTCAAACAATGGAAGGCATTTACTATCACATCCTTTTCGGGGAAAACAG	295		
Db	496	GCITCTATCCCGGAAGGAGC---GTCAGCTAATCTACACCCCATTCACAGAAGACACTG	552		
QY	296	ACAGTATCGTTGAGAAGGATTGATGTCACTTGGAAATGCTCTCTGCTCATGTTGTCGTGG	355		
Db	553	AGACTGTAGGCCAAAGAGCCCTGCATCGATCCTGAATCGCGGCCATCATGATCAGTGTCA	612		
QY	356	TCGTTCTGATGACAGTCTCTGCTGATTGTTTTCTATAAATACAAGTTTTATAAGCTTATTC	415		
Db	613	TTGTCAATTATGACCATCCTCCTGGTGGCTCTGTATAAATACAGTGTCTACAGGTCACTC	672		
QY	416	ATCGATGGCTTATGTGCACAGTTTCTTCTTCTTTTCCCTATTCACATACTATGTGC	475		
Db	673	ACGCCTGGCTTATTATTTCATCTCTGTGTCTGCTCTTTTTCGTTTCACTTTTACTTAG	732		
QY	476	AAGAAAGTCTGAAAGTTTTGATGTGTCTCCACAGCGCACTATTCGTTTGTTCGGACTGG	535		
Db	733	GGGAAGTATTTAGACCTACATGTGCGGTGGACTACGTTACAGTAGCACTTCCTAATCT	792		
QY	536	GTAACTATGGAGTTCTCGGAATGATGTGTATACATTGGAAAGGTCCATTGCGTCTGCAAC	595		
Db	793	GGAAATTTTGGTGTGTCGGGATGATTGCCATCCACTGGAAAGGCCCTTCGACTGCAGC	852		
QY	596	AGTTCTACCTTATTACAATGTCGCACTAATGGCTCTGGCTTTATCAAGTACCTACCAG	655		
Db	853	AGCGGTATCTCATATGATGACGTGCCCTTCATGGCCCCGTGTTATTATCAAGTACCTCCC	912		

QY	656	AATGACGTGTGGTTTGTGCTTTTGTATCTCGGTTGGGATCTGGTGGCCGTGCTCA	715
Db	913	AATGGACCGCATGGCTCATCTTGGCTGGAATTCAGTATATGATTTCGGTCTTTTAT	972
QY	716	CACCAAAAGGACCATTTGAGATATTTGGTGGAACTGCACAGGAGAGAAACGACCAATTT	775
Db	973	GTCCCAAGGCCACTTCGTATGCTGGTTGAAACAGCTCAGGAAGAAGAAATCAGACTCTCT	1032
QY	776	TCCCGGCGCTGATTTATTTTCGTCGTGGAGTCATCTACCTACGTTCTTGTTCACGCACTTG	835
Db	1033	TTCAGACTTTATCTATTTCTCAACATGGTGT---GGTGGTGAATATCGCTGAGGAG	1089
QY	836	AAACACACAGACACCCCGTGAACCGAGTCGTGCAGACTCAAACTCTACAGCTTTTC	895
Db	1090	ACCCAGAAAGCCCAAGGAGGTACCCAGAAACCCCAAGTATAACACACAAGAGCGGAGA	1149
QY	896	CTGGAGAGCGGAGTTGTTTCATCT--GAACGCCAAACGCCAAGGTGAACCAATTCCT	954
Db	1150	GAGACACAGACAGTGGTCTCGGGAACGATGTTGGCTTCAGTGGAGGATGGGAGG	1209
QY	955	CAAAAAGTGCAATCGAATCGAATPACAGCTTCAACGACACACAAAACCTCGAGTAAGG	1014
Db	1210	CCCAAGAGACAGTCACCTGGGGCTCATCGCTCCA-----	1245
QY	1015	GTGGAACGGGAGCTAGCTGCTGAGAGACCAACTGTACAAACGCCAATTTTCACAGGCAC	1074
Db	1246	---CTCCGAGTCAAGAGCTGTGTCACGGAACCTTTCGGGAGCATTTCAACGAGTGAA	1301
QY	1075	GAAGAGGAAGAGAGAGGTGTGAACCTTGGTCTCGGGACATTCATTTCTACTCTGTCTC	1134
Db	1302	GACCCGGAGAAAGAGCAGTAAACCTTGGACTGGAGATTTTCATTTTCTACAGTGTCTG	1361
QY	1135	CTCGGCAAGGCTTCATCGTACT-----TTGACTGGAACACGACTATCGCTTGTATTG	1188
Db	1362	GTTGGTAAGGCTCTAGCAACGCCAGCTGGAGACTGGAACACCAACCATAGCTGCTTTGTA	1421
QY	1189	GCCATCTTATCGGCTCTCTCTTCACTCTGTCTCGCGCTCTTTCAAGACGACATC	1248
Db	1422	GCCATCTGATCGGCTGTCCCTTACATTACTCTCTCTCGCCATTTTCAAGAAAGGTTG	1481
QY	1249	CCGGCTCT--CAATTTCCATTTTCTCCGAGCTCATTTTTCATTT	1291
Db	1482	CCAGCCCTCCCATCTCCACACTTTCGAGCTCGTGGCTCTGTCTCTACTT	1525

RESULT	37
AR087310.	
LOCUS	AR087310
DEFINITION	Sequence 135 from patent US 5986054.
ACCESSION	AF087310
VERSION	AR087310.1 GI:10014073
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unclassified. Unclassified.
REFERENCE	1 (bases 1 to 1962)
AUTHORS	St. George-Hyslop P.H., Rommens,J.M. and Fraser,P.E.
TITLE	Genetic sequences and proteins related to alzheimer's disease
JOURNAL	Patent: US 5986054-A l35 l6-NOV-1999;
FEATURES	Location/Qualifiers 1..1962 /organism="unknown"
source	
BASE COUNT	503 a 503 c 496 g 460 t
ORIGIN	

Query Match	16.2%	Score 243.2	DB 6	Length 1962
Best Local Similarity	54.4%	Pred. No. 4.2e-45		
Matches 644	Conservative	0	Mismatches 498	Indels 42
			Gaps 6	
QY	116	AGAAGACGAAATATGTTGTGGAAGACGCGAGCTGAAATACGGAGCATCTCACGTTATTC	175	
Db	376	ACAAGATGAGGAGGAAGACGAGAGCTGCATTTGAAATATGAGCCCAAGCATGTCATCA	435	

QY 776 TCCCGCGCTGATTATTTATTCGTCCTGAGTCACTATCCCTACGTTCTTGTACTCCAGTTG 835
 Db 1033 TTCAGCTCTTATCTATTCCTCAACAATGGTGT---GGTTGGTGAATATGCTGAAGGAG 1089
 QY 836 AAAACACACAGACAGACCCCGTGAACCGAGCTCGTCAGACTCAAACTCTTACAGCTTTTC 895
 Db 1090 ACCCAGAGGCCAAGAGAGGTACCCAAAGACCCCAAGTATACACAAAGACGGGAGA 1149
 QY 896 CTGAGAGGGGAGTTGTTCTATCT---GAAACGCCAAACCGGCCAAAGTGAACAGAAATTCCT 954
 Db 1150 GAGACACACAGACAGTGGTTCTGGGAACGATGATGGTGGCTTCAGTGAGAGTGGGAGG 1209
 QY 955 CAAAAAGTGAACAAATCGAATCGAATCTACACTTCAAGACACAAACTCTGGAGTAGG 1014
 Db 1210 CCAAGAGACAGTCACTCGGGGCTCATCGCTCCA----- 1245
 QY 1015 GTGAAGGGGAGCTAGCTGTGAGAGACCAACTCTACAAGACGGCAATTTTCAGAGCAC 1074
 Db 1246 ---CTCCGAGTCAAGAGCTGTGTCCAGGAATTTCTGGGAGCATTTCAACGAGTGAA 1301
 QY 1075 GAAGAGAGAGAGAGTGTGAACACTTGGTCTGGGCGACTTCAATTTTCTACTCTGTCTC 1134
 Db 1302 GACCCGAGGAAGAGAGAGTAAACTTGGACTGGGAGATTTCAATTTTCTACAGTGTCTG 1361
 QY 1135 CTCGGCAAGGCTTCATCGTACT-----TTGACTGGAACAGCACTATCGCTGTGTATGTG 1188
 Db 1362 GTTGGTAAGCCCTCAGCAACCGCCAGTGGAGACTGGGAACACACCATAGGCTGTGTGTA 1421
 QY 1189 GCCATTTCTATCGGTCT 1248
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 QY 1249 CCGGCTCT-GCAATTTCCATTTCTCGGACTCATTTTACTT 1291
 Db 1482 CCAGCCCTCCCATCTCCATCACTTCGCGCTCGTGTCTACTT 1525
 RESULT 39
 ARI44598
 LOCUS ARI44598 1964 bp DNA linear PAT 08-AUG-2001
 DEFINITION Sequence 135 from patent US 6210919.
 ACCESSION ARI44598
 VERSION ARI44598.1 GI:15106465
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1964)
 AUTHORS St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E.
 TITLE Genetic sequences and proteins related to Alzheimer's disease
 JOURNAL Patent: US 6210919-A 135 03-APR-2001;
 FEATURES Location/Qualifiers
 source 1..1964
 BASE COUNT 503 a 503 c 496 g 460 t 2 others
 ORIGIN
 Query Match 16.2%; Score 243.2; DB 6; Length 1964;
 Best Local Similarity 54.4%; Pred. No. 4.2e-45;
 Matches 644; Conservative 0; Mismatches 498; Indels 42; Gaps 6;
 QY 116 AAGAAGACGAAATGTTGGAGAGAGCGGAGTGAATACGAGCATCTCAGCTTATTC 175
 Db 378 AACAGATGAGGAGGAGGAGGAGAGCTGACATTTGAATATGAGCAAGCATGTCA 437
 QY 176 ATCTATTCTGCGGTGTCATATGATGCTGTGTTGTTTACGATGACACAGATTA 235
 Db 438 TGCCTCTTGTCCCGGTGACCCCTGTGCATGGTGTGCTGTGGCCACCATCAATCAGTCA 497
 QY 236 CGTTTATAGTCAAAACAATGGAAGGCATTTTACTATCATCATCTTTTCGCGGGAACAG 295
 Db 498 GCTTCTATACCCGGAAGGAGG---GTCAGCTAATCTACACCCCATTCACAGAAGACACTG 554

RESULT 40

MUSSI1P

LOCUS

QY 296 ACAGTATCGTTGAGAGAGGATGATGTCACCTTGGAAATGCTCTCGTCATCTGTTGCGCTGG 355
 Db 555 AGACTGTAGGCCAACAGAGCCCTGCACCTGATCTCTGAATGGGCATCATGATCAGTGTCA 614
 QY 356 TCCTTCTGATGACAGTCTCTGATCTGTTTCTTATATAAACAAGTTTATATAAGCTTATTC 415
 Db 615 TTGTCAATATGACCATCTCTCTGCTGCTGTATATAAATACAGGTGCTACAGGTCAATCC 674
 QY 416 ATGATGAGCTTATTTGTCAGCAGTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 475
 Db 675 ACCTGCTCTTATTTATTTCT 734
 QY 476 AAGAAGTCTTGAAGTTTCGATGTGTCTCCAGCGCAGCTATTTGGTTTCTTTTGGACTGG 535
 Db 735 GGAAGATTTTAAAGACCTACAATGTCTGCGCTGGACTACGTTACAGTACAGTCTCTATCT 794
 QY 536 GTAACTATGAGATTCCTCGGAATGATGTATATGAAAGGTCCATTCGCTCGTCAAC 595
 Db 795 GGAATTTTGTGTGGTGGGATGATGCTCATCTGGAAGGCCCTTCGACTCGAGC 854
 QY 596 AGTCTACCTTATTAACAATGTCTGCACATAATGGCTCTGGTCTTTTATCAAGTACCTACCAG 655
 Db 855 AGCGTATCTCATTTATGATCAGTCCCTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 914
 QY 656 AATGGACTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 715
 Db 915 AATGGACCGCATGGCTCATCTTGGCTGTGATTTTCACTATATGATTTTGGTGGCTTTTAT 974
 QY 716 CACAAAAGGACCATTTGATGATATTTGGTGAAGTCTGCACAGGAGAGAAAGAGCCCAATTT 775
 Db 975 GTCCAAAGGCCACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1034
 QY 776 TCCCGGCGTGATTTATTCGCTGAGTCACTATCTATCCCTACGTTCTTGTGTCAGTTG 835
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 QY 836 AAAACACGACAGACCCCGTGAACCGAGCTGTCAGACTCAATATCTTCTACAGCTTTTC 895
 Db 1092 ACCGAGAGCCCAAGAGGGTATCCCAAGAACCCCAAGTATAACACACAAAGAGCGGAGA 1151
 QY 896 CTGGAGAGCGGAGTTGTTCATCT-GAAAGGCCAAAACGGCCAAAAGTGAACCAATTCCT 954
 Db 1152 GAGAGACACAGGACAGTGGTTCTGGAAGCATGATGCTGCTTCACTGAGGAGTGGGAGG 1211
 QY 955 CAAAAAGTGAATCGAATCGAATCTACAGCTTCAACGACACAAACTCTCTGGAGTAAGG 1014
 Db 1212 CCAAAAGACACAGTCACTGGGCTCATCTGCTCCA----- 1247
 QY 1015 GTGGAACGGGAGTCTGCTGAGACCAACTGTACAAGACCCCAATTTTCACAGGCAC 1074
 Db 1248 ----CTCCCGAGTCAAGAGCTGCTGTCCAGGAATTTCTGGGAGCAATTTACAGGTGAA 1303
 QY 1075 GAAGAGAAAGAGAGGTTGTGAACCTTGGTCTGGGCACTTCAATTTCTACTCTGTCTC 1134
 Db 1304 GACCCGAGGAAAGAGGAGTAAACCTTGACCTGGGAGATTTCTATTTCTACAGTGTCTG 1363
 QY 1135 CTCGGCAAGGCTTCATCTGCTACT-----TTGACTGGAACAGCACTATCTCTGTTATGTG 1188
 Db 1364 GTTGTGAAGGCTTCAGCAACCCCGAGTGGAGACTGGAACACCAACCATACCTGCTTTGTA 1423
 QY 1189 GCATTTCTATCGGTCTCTGCTTCTACTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1248
 Db 1424 GCCATCTGATCGGCTGTGCTTACATTTACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1483
 QY 1249 CCGGCTCT-GCAATTTCCATTTTCTCGGACTCATTTTACTT 1291
 Db 1484 CCAGCCCTCCCATCTCTCATCATCTTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1527

1964 bp

mRNA

linear

ROD 24-JUL-1995

835 GAAACACGACAGACCCCGTGACCGAGCTGTCAGACTCAATACTCTTACAGCTTTT 894

PLSNGRPOGNSRQVVEQDEDEBELTKYGAHVIMLFVPTLCMVVVVATIKSVSY
TRDQDIYPTTETVGOALHSILNAAIMSVIVVMTILLVLYKYRCYKVIHA
WLIISLLLFYFFSFIYGEVFTYINVAVDYITVALLIWNFVVGMTSIHWKGLRQ
QAYLIMISALMALVFIKYLPEWTLALIVSVVDIVAVLCPKPLRMLVETAEERNE
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1126. 1484
/gene="AD3-212"

3'UTR
BASE COUNT 373 a 343 c 357 g 411 t

Query Match 15.9%; Score 239; DB 9; Length 1484;
Best Local Similarity 60.5%; Pred. No. 3.8e-44;
Matches 411; Conservative 0; Mismatches 265; Indels 3; Gaps 1;

QY	119	AAGACGAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCAGCTTATTCATC	178
Db	182	AAGATGAGGAAGAAGATGAGGAGCTGACATGAATATGATGCGCAAGCATGTGATATGC	241
QY	179	TATTGTCCGGTGTCTACTATGATGGCTCTGGTGTGTTTACGATGAACAGGATACGT	238
Db	242	TCITTTGCCGTGACTCTCTGATGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	301
QY	239	TTTATAGTCAAAACATGGAAGCAATTTACTATACATCTCTTTTGTCCGGGAACAGACA	298
Db	302	TTTATACCGGAAGGATG---GGACGCTATCTATACCCCAATTCACAGAAGATACCGAGA	358
QY	299	GTATCGTTGAGAGGATGATGATCTACTTGGAAATGCTCTCGCTGCTGCTGCTGCTGCTG	358
Db	359	CTGTGGCCAGAGAGCCCTGCACCTCAATCTGATGCTGCCATCATGATGATGATGATG	418
QY	359	TTCTGATGACAGTTCTGCTGATGTTTCTATAAATACAAGTTTATAAGCTTTATTCATG	418
Db	419	TTGTCATGACTATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	478
QY	419	GATGGCTTATGTCAGCAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	478
Db	479	CTGGCTTATATATATCATCTATGTTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT	538
QY	479	AGATCTGAAAAGTTTCGATGTCTCTCCAGCGCCTATTTGTTTGTGGAGCTGGGTA	538
Db	539	AAGTGTAAAACCTATAACGTTGCTGTGGACTACATTAATGCTGCTGCTGCTGCTGCTG	598
QY	539	ACTATGGAGTTCTCGAATGATGTATACATTTGAAAGGTCATTTGCTGTGCAACAGT	598
Db	599	ATTTTGGTGTGGGATGATTTCCATTCATCTGGAAGGTCCTGCTGCTGCTGCTGCTGCT	658
QY	599	TCTACTTATTAACAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	658
Db	659	CATATCTATATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	718
QY	659	GGACTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	718
Db	719	GGACTGTGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	778
QY	719	CAAAAGGACCATGATATTTGGTGAACATGACAGAGAGAGAAACAGGACCAATTTTCC	778
Db	779	CGAAAGGACCATGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	838
QY	779	CGGCGCTGATTTATTCGTC	797
Db	839	CAGCTCTCATTTACTCTCTC	857

RESULT 45
AY043493
LOCUS 1430 bp mRNA linear VRT 02-SEP-2001
DEFINITION Gallus gallus presenilin 2 mRNA, complete cds.
ACCESSION AY043493
VERSION AY043493.1 GI:15421098
KEYWORDS Gallus gallus.
SOURCE Gallus gallus
ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 1430)
Korade Mirnics,Z., Keryanov,S., Lovelock,J. and Corey,S.J.
Cloning of chicken presenilins
Unpublished
2 (bases 1 to 1430)
Korade Mirnics,Z., Keryanov,S., Lovelock,J. and Corey,S.J.
Direct Submission
Submitted (04-JUL-2001) Pediatrics, Children's Hospital of
Pittsburgh, University of Pittsburgh, 3460 Fifth Avenue,
Pittsburgh, PA 15213, USA
FEATURES
Location/Qualifiers
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47..1402
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BASE COUNT 377 a 332 c 335 g 380 t 6 others

Query Match 15.9%; Score 238.2; DB 5; Length 1430;
Best Local Similarity 60.1%; Pred. No. 5.8e-44;
Matches 412; Conservative 0; Mismatches 270; Indels 3; Gaps 1;

QY	124	GAAATGTTGTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCAGCTTATTCATCTATT	183
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QY	184	GTGCGGTGTCTACTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	243
Db	341	GTGCGGTGTCTACTATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	400
QY	244	AGTCAAAACAATGGAAGCATTACTATACATCTCTTTTGTCCGGGAACACACAGATATC	303
Db	401	ACGGAGAAAAGC---GGCAGCTGATCTACACCCCTTTTCAGTGAGGACACCCCATCCG	457
QY	304	GTGGAAGAAGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	363
Db	458	GGCCAGCGCTCTTCAACTCAGTGTGAACACTATCAATATGATCAGGCTCATCTGTA	517
QY	364	ATGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	423
Db	518	ATGACAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	577
QY	424	CTTATTGTGACAGTTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	483
Db	578	CTAATCTGCT	637
QY	484	CTGAAAAGTTTCGATGTCTCTCCAGCGCCTATTTGTTTGTGGACTGGTAACATAT	543
Db	638	TTGAAGACATACATGTTGGCCATGATTAACCCACAGTATCTTAATCATCTCGAATTTT	697
QY	544	GGAGTTCTCGAATGATGTATACATTTGAAAGGTCCATTTCCGCTGCAACAGTTCTAC	603
Db	698	GGAGTTCTGGAATGATTCGCATCCACTTGAAGGTCCCTTTCGAGCTCCAGCAAGCAT	757
QY	604	CTTATTACAATGTCTGCACATTAATGGCTCTGCTCTTTTATCAAGTACCTACCAGATG	663

Db	371	CTGTGGGCCAGGGAGCCCTGCATCTGAATCTGCCATCATGATCAGTGTCAATG	430
Qy	359	TTCTGATGACAGTCTTCTGCTGATGTTTTCTATAAATACAAGTTTTATAAGCTTATTCATG	418
Db	431	TTGTCAATGACTATCCTCTCGTGGTGTTCTGTATAAATACAGGCTATATAAGGTCATCCATG	490
Qy	419	GATGGCTTATGTGCACAGTTTTCTTCTTTTCTTTTCTTATTCACATACATCTATGTGCAAG	478
Db	491	CCTGGCTATTATATCATCTATTTGTTGCTGTCTTTTTCATTCAATTTACTTTGGGGG	550
Qy	479	AAGTCTCTGAAAGTTTTCGATGTCTCCACCGCACTATTGGTTTTGTTGGACTGGGTA	538
Db	551	AAGTGTTTAAACCTTAAAGTGTCTGGACTACATTTACTTCTGCACCTCTGATCTGGA	610
Qy	539	ACTATGGAGTCTTCGGAATGATGTATACATTGGAAGTCCCAATTCGCTGCAACAGT	598
Db	611	ATTTTGGTGTGGTGGGAATGATTTCCATTCACCTGGAAGTCCACTTCGACTCCACGAG	670
Qy	599	TCTACCTTATACAATGCTGCACATAATGGCTCTGGTCTTTATCAAGTACCTTACCAGAAT	658
Db	671	CATATCTCATATGATTAAGTGCCTCATGGCCCTGGTGTATTATCAAGTACCTCCCTGAAT	730
Qy	659	GGACTGTGGTGTGTGTGTTTATCTCGGTTTGGGATCTGGTTCGGTCTCACAC	718
Db	731	GGACTGCGTGGCTCATCTTGGCTGTGATTTCCGTATATGATTTAGTGGCTGTTTTGTGTC	790
Qy	719	CAAAAGGACCAATTCAGATATTTGGTGGAACTGCACAGGAGAAACGACCAATTTTCC	778
Db	791	CGAAGGTCACACTTCGTATGCTGGTTGAAACAGCTCAGGAGAAATGAACGCTTTTC	850
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316 a 287 c 322 g 329 t

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Query Match      15.8%; Score 237.4; DB 9; Length 1254;
Best Local Similarity 60.4%; Pred: No. 8.9e-44;
Matches 410; Conservative 0; Mismatches 266; Indels 3; Gaps 1;

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194 AGATGAGGAAGAAGATGAGGAGCTGCAUATGAAATATGCGCCAGCATGTGATCATGC 253
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179 TATTTGTGCCGTGTCACTATGTCATGCTCTGGTGTGTTTTACGATGAACAGATTACGT 238
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254 TCTTTGTCCCTGTGACTCTCTGCATGTTGGTGTGGCTACCAATTAAGTCAGTCAGCT 313
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239 TTTATAGTCAAAACAATGGAGGCAATTTACTACATCCTTTTGTCGGGAAACAGACA 298
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
314 TTTATACCGGAAGATG---GGCAGCTAATCTATACCCCAATTCACAGAAGATACCGAGA 370
      ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
299 GTATCGTTGAGAAGGGGATTGATGTCACTTGGAAATGCTCTCGTCATGTTGTGCGTGGTCG 358
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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116	QY	AGAAAGCAGAAAATGTTGGAAGAAGCGGAGCTGAAATACGGAGCATCTCAGGTTATTC	175
378	Db	AAACAATGAGGAGGAAGACGAAGCTGACATTCAATATGGAGCCAAGCATGTCAATCA	437
176	QY	ATCTATTCTCCGGTGTCTACTATGCATGCGTCTGGTTGTTTTACGAATGAACACGATTA	235
438	Db	TGCTCTTTGTCCCGTGACCTCTGCATGGTCTGCTGCTGGCGCCACCATCAATCAAGTCA	497
236	QY	GCTTTTATGACAAAACAAATGGAAGGCATTTACTATCACATCCTCTTTTCTCCGGCAACAG	295
498	Db	GCTTCTATACCGGAAGGACG--GTCAGCTAACTACACCCCAATTCACAGAAGCACTG	554
296	QY	ACAGTATCGTTGAGNAGGATGATGTCACATTTGGAATGCTCGTCATGTTGCGGTGG	355
555	Db	AGACTGTAGGCCAAGAGCCCTGCACCTCGATCCTTGAATGGGCCATCATCAGTGCTCA	614
356	QY	TCGTTCTGATGACAGTTCCTGCTGATGTGTTTCTATAAATACAAGTTTTATAAGCTTATTC	415
615	Db	TTGTCATTATGACCATCCTCTCTGCTGCTCTGTATAAATACAGGTGCTACAGGTCAATCC	674
416	QY	ATGGATGGCTTATTGTCAGCAGTTTCTCTCTCTTTTCCCTATTTCACCTACAACTATATGTC	475

RESULT 50	REFERENCE
AR144468	AUTHORS
LOCUS	TITLE
DEFINITION	JOURNAL
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	

AR144468 1929 bp DNA linear PAT 08-AUG-2001
Sequence 3 from patent US 6210919.
AR144468
AR144468.1 GI:15106335
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Unknown.
Unknown.
Unclassified.
1 (bases 1 to 1929)
St. George-Hyslop, P.H., Rommens, J.M. and Fraser, P.E.
Genetic sequences and proteins related to alzheimer's disease
Patent: US 6210919-A 3 03-APR-2001;

FEATURES	Location/Qualifiers
source	1. .1929
BASE COUNT	/organism="unknown"
ORIGIN	489 a 494 c 490 g

Query Match	15.6%;	Score 233.6;	DB 6;	Length 1929;
Best Local Similarity	53.6%;	Pred. No. 6.6e-43;		
Matches 635; Conservative	2;	Mismatches 505;	Indels 42;	Gaps 6;

QY	116	AAGAAGACGAATATGTTGTGGAAGACGGAGCTGAAATACGGAGCATCTCAGCTTATTC	175
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QY	176	ATCTATTGTCCGGTGCACATATGCATGGCTCTGGTTGTTTTACGATGAACAGATTA	235
Db	438	TGCTCTTTGTCGCCGTGACCCCTTCGATGGTGTGCTGTGGCCACCATCAAAATCAGTCA	497
QY	236	CGTTTTATAGTCAAAACAATGGAAGGCAATTTACTATACATCTCTTTTCTCCGGGAACAG	295
Db	498	GCTTCTATACCCGGAAGGACG--GTCAGCTAACTACACCCATTACAGAGACACTG	554
QY	296	ACAGTATCGTTGAGAAGGATGTGATGTCACTTGGAAATGCTCTCGTCAATGTGTGCGTGG	355
Db	555	AGACTGTAGGCCAAAGAGCCCTGCATCGATCCCTGAATCGCGCCATCATGATCATGTGCA	614
QY	356	TCGTTCTGATCACAGTGTCTGTGATGTGTTTCTATAAATACAAGTTTTATAGCTTATTC	415
Db	615	TTGTCATTATGACCATCTCTCGTGGTCCCTGTATAAATACAGGTGCTACAAGTGCATCC	674
QY	416	ATGGATGGCTTATTTGTGACGAGTTTTCTTCTCTTTTCTTCTATTCACATACTATGTC	475
Db	675	ACGCTGGCTTATTATTTCATCTCTGTGTGTGCTTCTTTTTTTCGTTTACATTACITAG	734
QY	476	AAGAAGTCTCAAAAGTTTCGATGTGTCCTCCAGGGCACTATTTGGTTTTGTTGGACTGG	535
Db	735	GGGAAGTATTTAAGACCTACAAATGTCCKCGTGGACTAGTTTACAGTAGCACTCTCTAA	794
QY	536	GTAAGTATGAGTTCTCGGAATGATGTATACATTTGGAAGGTCCATTGGCTGTGCAAC	595
Db	795	GGAATGGGGTGTGGTCCGGATGATGCCATCCACTGGAAGGCCCTTCGACTGCGACG	854
QY	596	AGTTCTACCTTATPACAATGTCTGCACATAATGGCTCTGGTCTTTATCAAGTACCTAC	655
Db	855	AGGCGTATCTCAATTATGATCAGTCCCTCATGGCCCTGGTATTATCAAGTACCTCCCG	914
QY	656	AATGGACTGTCTGTTTTGCTGTGTTGTATCTCGGTTTGGGATCTGGTTCGCGTGCTCA	715
Db	915	AATGGACCGCATGGCTCATCTTGCTGTGATTTTCAGTATATGATTTGGTGGCTGTTTAT	974
QY	716	CACCAAAGACCAATTCAGATATTTGGTGGAACTGCACAGGAGAGAAACGACCAATTT	775
Db	975	GTCCCAAGGCCCACTTCGTATGCTGTTGAAACAGCTCAGGAAGAAATGAGACTCTCT	1034
QY	776	TCCGGGGCTGATTTATTTGCTGGAGTCACTATCTCCCTAGTTCCTTTGTTACTCAGTTG	835
Db	1035	TTCCAGCTCTTCTATTTCCTCAACAATGGTGT---GGTGGTGAATATGCTCAAGGAG	1091
QY	836	AAAACAGCAGACAGCCCCGTGAACCGACGTCTGCAGACTCAATATCTTACAGCTTTTC	895
Db	1092	ACCCAGAGCCCAAGAGGAGGTACCCAGAACCCTCAAGTATTAACACACAAGACGGAGA	1151
QY	896	CTGGAGAGGGGAGTTGTTCATCT--GAAACGCCAAAACGGCCAAAAGTGAACGAATTCCT	954
Db	1152	GAGAGACACAGGACATGGTTCTGGGAAACCATGATGTTGGCTTCAGTGAAGATGGGAGG	1211
QY	955	CAAAAAGTGCAAATCGAATCGAATACTACAGCTTCAACAGCACACAAAACCTCTGGAGTA	1014
Db	1212	CCCAAGAGACAGTCACTGGGGCTCATCGCTCCA-----	1247
QY	1015	GTGGAAGGGGAGCTAGCTGCTGAGAGACCAACTGTACAAACGCCCAATTTTCACAGCAC	1074
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Search completed: July 15, 2003, 08:17:48
Job time : 4016 secs

Qy	1075	GAAGAGGAGAGAGAGGTGTGAACCTTTGGTCTGGCGACTCAATTTCTACTCTGTTC	1134
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Qy	1249	CCGGCTCT-GCAATTTCCATTTTCTCCGACTCAATTTTACTT	1291
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